

MicroRNA Expression Profiles in Cultured Human Fibroblasts in Space

Honglu Wu¹, Tao Lu^{1,2}, John Jeevarajan³, Larry Rohde² and Ye Zhang^{1,4}

¹NASA Johnson Space Center, Houston, Texas

²University of Houston Clear Lake, Houston, Texas

³Northwestern University, Chicago, Illinois

⁴Wyle Laboratories, Houston, Texas

Microgravity, or an altered gravity environment from the static 1g, has been shown to influence global gene expression patterns and protein levels in living organisms. However, it is unclear how these changes in gene and protein expressions are related to each other or are related to other factors regulating such changes. A different class of RNA, the small non-coding microRNA (miRNA), can have a broad effect on gene expression networks by mainly inhibiting the translation process. Previously, we investigated changes in the expression of miRNA and related genes under simulated microgravity conditions on the ground using the NASA invented bioreactor. In comparison to static 1 g, simulated microgravity altered a number of miRNAs in human lymphoblastoid cells. Pathway analysis with the altered miRNAs and RNA expressions revealed differential involvement of cell communication and catalytic activity, as well as immune response signaling and NGF activation of NF- κ B pathways under simulated microgravity condition. The network analysis also identified several projected networks with c-Rel, ETS1 and Ubiquitin C as key factors. In a flight experiment on the International Space Station (ISS), we will investigate the effects of actual spaceflight on miRNA expressions in non-dividing human fibroblast cells in mostly G1 phase of the cell cycle. A fibroblast is a type of cell that synthesizes the extracellular matrix and collagen, the structural framework for tissues, and plays a critical role in wound healing and other functions. In addition to miRNA expressions, we will investigate the effects of spaceflight on the cellular response to DNA damages from bleomycin treatment.